

57661
SEARCH REQUEST FORM

Requestor's

Name: Bronwen Loeb

Serial

Number: 09/635,521Date: 1/7/02Phone: 605-1197Art Unit: 1636MAILBOX: 11 E 12OFFICE: 12 D 12**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search the commercial
nucleotide databases for Seq ID No. 1
and the commercial protein databases
for Seq ID No. 2

Edward Hart
Technical Info Specialist
STIC / Biotech
CM1 12C14 Tel: 305 9203

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1/8/02
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Searcher: _____

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Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

☒ STIC☒ CM-1☐ Pre-S

Type of Search

☒ N.A. Sequence☒ A.A. Sequence☐ Structure☐ Bibliographic

Vendors

☐ IG☐ STN☐ Dialog☐ APS☐ Geninfo☐ SDC☐ DARC/Questel☒ Other

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 8, 2002, 23:04:10 ; Search time 24.21 Seconds
(without alignments)
686.046 Million cell updates/sec

Title: US-09-635-521a-2

Perfect score: 2334
Sequence: 1 MASPSLPGSDCSQIIDSHV.....NSGAKPANSANGFQEHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	23.34	100.0	453 1	GP39_HUMAN
2	481.5	20.6	424 1	NTF1_MOUSE
3	473	20.3	424 1	NTF1_RAT
4	466.5	20.0	418 1	NTF1_HUMAN
5	419	18.0	416 1	NTF2_RAT
6	404	17.3	410 1	NTF2_HUMAN
7	401.5	17.2	417 1	NTF2_MOUSE
8	355.5	15.2	412 1	GP38_HUMAN
9	310	13.3	366 1	GHSR_PIG
10	308	13.2	364 1	GHSR_RAT
11	299	12.8	366 1	GHSR_HUMAN
12	273.5	11.7	380 1	APJ_MACMU
13	272.5	11.7	380 1	APJ_HUMAN
14	267.5	11.5	377 1	APJ_MOUSE
15	263.5	11.3	444 1	OX2R_HUMAN
16	259.5	11.1	441 1	ETBR_BOVIN
17	259.5	11.1	564 1	5HT1_DROME
18	258	11.1	346 1	GALR_RAT
19	256.5	11.0	363 1	SSR3_RAT
20	255	10.9	388 1	5H4_MOUSE
21	254	10.9	348 1	GALR_MOUSE
22	253.5	10.9	444 1	OX2R_CANFA
23	252.5	10.8	444 1	SSR3_RAT
24	252	10.8	362 1	SSR5_MOUSE
25	252	10.8	362 1	TRFR_CHICK
26	250.5	10.7	398 1	TRFR_SHEEP
27	250.5	10.7	428 1	SSR3_MOUSE
28	250.5	10.7	443 1	ETBR_PIG
29	250	10.7	349 1	GALR_HUMAN
30	249.5	10.7	398 1	TRFR_HUMAN
31	249.5	10.7	427 1	ETIR_BOVIN
32	249.5	10.7	470 1	ALIA_ORILA
33	248.5	10.6	398 1	TRFR_BOVIN

34	248.5	10.6	426 1	ETIR_RAT	P26684	rattus norv
35	248	10.6	460 1	OX2R_RAT	P56719	rattus norv
36	247.5	10.6	401 1	OPRM_PIG	O95247	sus scrofa
37	247.5	10.6	412 1	TRFR_RAT	O01717	rattus norv
38	246.5	10.6	418 1	SSR3_HUMAN	P32745	homo sapien
39	245.5	10.5	427 1	ETIR_HUMAN	P23101	homo sapien
40	244.5	10.5	427 1	ETBR_COTJA	O90328	coturnix co
41	244.5	10.5	427 1	ETIR_PIG	O29010	sus scrofa
42	244	10.5	391 1	SSRI_HUMAN	P30872	homo sapien
43	244	10.5	391 1	SSRI_MOUSE	P30873	mus musculu
44	244	10.5	391 1	SSRI_RAT	P28646	rattus norv
45	243.5	10.4	393 1	TRFR_MOUSE	P21761	mus musculu

ALIGNMENTS

RESULT 1	GP39_HUMAN	STANDARD;	PRT;	453 AA.
ID	GP39_HUMAN			
AC	O43194;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39.			
GN	GPR39.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RC	MELINE=98110578; PubMed=9441746;			
RX	McGee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D., Hreniuk D.L., Smith R.G., Howard A.D., Van der Ploeg L.H.T.; "Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors.";			
RT	Genomics 46:426-434(1997).			
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: AF034633; AAC26082.1; "			
CC	CCRPdb: GCR.2493; "			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Plan: PF00001; Tm1; 2.			
DR	PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.			
DR	PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.			
DR	G-protein coupled receptor; Transmembrane; Glycoprotein.			
KW	DOMAIN 1			
FT	DOMAIN 1			
FT	TRANSMEM 26			
FT	TRANSMEM 47			
FT	DOMAIN 72			
FT	TRANSMEM 93			
FT	DOMAIN 110			
FT	TRANSMEM 132			
FT	DOMAIN 155			
FT	TRANSMEM 176			
FT	DOMAIN 224			
FT	TRANSMEM 244			
FT	DOMAIN 281			
FT	TRANSMEM 302			
FT	DOMAIN 321			
FT	TRANSMEM 347			

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CC DOMAIN 348 428 CYTOPLASMIC (POTENTIAL).
FT DISULFID 108 210 BY SIMILARITY.
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 453 AA: 51328 MW; 8E3A233420D9021E CRC64;

Query Match
Best Local Similarity 100.0%; Score 2334; DB 1; Length 453;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASPSLPGSDCSQIIDHSHVPEFEVAWIKITLLVYLIFVWGLGNSAATRYQVLQK 60
DB 1 MASPSLPGSDCSQIIDHSHVPEFEVAWIKITLLVYLIFVWGLGNSAATRYQVLQK 60
QY 61 KGYLKEVYDHWVSLACSDILVFLGMPPEFYSITWNPULTSSYTLSCKLTPEACSY 120
DB 61 KGYLKEVYDHWVSLACSDILVFLGMPPEFYSITWNPULTSSYTLSCKLTPEACSY 120
QY 121 ATLLHVLTLSEFERYTALCHPFRYKAVSGPCQYKLLIGFVWVTSALVALPLLFAMGTEYPL 180
DB 121 ATLLHVLTLSEFERYTALCHPFRYKAVSGPCQYKLLIGFVWVTSALVALPLLFAMGTEYPL 180
QY 181 VAVPSHRLGTCRRSTRHHEOPEFETSMGICTLTSRMTVFOSSTIGARVYLVLSYAF 240
DB 181 VAVPSHRLGTCRRSTRHHEOPEFETSMGICTLTSRMTVFOSSTIGARVYLVLSYAF 240
QY 241 MCMNMAYVLMSQKSLAGTRPPOLRKSESESESTARRQTIIFLLVYLAVCWMPNQ 300
DB 241 MCMNMAYVLMSQKSLAGTRPPOLRKSESESESTARRQTIIFLLVYLAVCWMPNQ 300
QY 301 IRRIMAAPKPKHDMTRSYFRAYMILLPSETFEYLSVINPLLYTVSSQGFRRVQVYL 360
DB 301 IRRIMAAPKPKHDMTRSYFRAYMILLPSETFEYLSVINPLLYTVSSQGFRRVQVYL 360
QY 361 CRLSLQHNHKEKRLVHAHSTDSARFVORPLLFASROSSARREKTELFSTPQSEAPQ 420
DB 361 CRLSLQHNHKEKRLVHAHSTDSARFVORPLLFASROSSARREKTELFSTPQSEAPQ 420
QY 421 SKQSLSLESLPEPNSGAKPANSAAENGQEHV 453
DB 421 SKQSLSLESLPEPNSGAKPANSAAENGQEHV 453

RESULT 2
NTRI_MOUSE STANDARD; PRT; 424 AA.
A 088319;
D 20-AUG-2001 (Rel. 40, Created)
D 20-AUG-2001 (Rel. 40, Last sequence update)
D 20-AUG-2001 (Rel. 40, Last annotation update)
D NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1).
D NTSLR OR NTSR.
D Mus musculus (Mouse).
D Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
D Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
D NCBI_Taxid=10090.
R 11
R SEQUENCE FROM N.A.
R TISSUE=Brain;
R Snider J., Sano H., Ohta M.;
R "Neurotensin receptor type 1."
R submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
R -1- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
R ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
R CALCIUM SECOND MESSENGER SYSTEM.
R -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
R -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
R HIGHEST TO TACHIKININS RECEPTORS.
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CC -----
DR EMBL: AB017027; BAA33013.1; -.
DR MGD: MGI:97386; Ntsr.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECP_F1.1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW phosphorylation; lipoprotein; Palmitate.
FT DOMAIN 1 64
FT TRANSSEM 65 87
FT DOMAIN 88 96
FT TRANSSEM 97 121
FT DOMAIN 122 143
FT TRANSSEM 144 165
FT DOMAIN 166 188
FT TRANSSEM 189 210
FT DOMAIN 211 235
FT TRANSSEM 236 260
FT DOMAIN 261 308
FT TRANSSEM 309 330
FT DOMAIN 331 348
FT TRANSSEM 349 372
FT DOMAIN 373 424
FT CARBOHYD 4 4
FT CARBOHYD 38 38
FT CARBOHYD 42 42
FT CARBOHYD 211 211
FT DISULFID 141 224
FT LIPID 388 388
SQ SEQUENCE 424 AA: 47216 MW; 8E9A723171A48711 CRC64;

Query Match
Best Local Similarity 20.6%; Score 481.5; DB 1; Length 424;
Matches 123; Conservative 73; Mismatches 165; Indels 59; Gaps 9;

QY 8 GSDCSQIIDHSHVPEFEVAWIKITLLVYLIFVWGLGNSATRYQVLQKGR--IQ 65
DB 41 GNSSESTLEPNSMLDVNTDIYSKVLAVYALFVVGTVGNSVT--AFLARKSLQSLQ 98
QY 66 KEVTDHWVSLACSDILVFLGMPPEFYSITWNPULTSSYTLSCKLTPEACSYATLLH 125
DB 99 STYHHLGSLALSDLLILLAMPVELLNFVWHHPAFGAGCGRYFLRDACVATFALN 158
QY 126 VTLSEFERYTALCHPFRYKAVSGPCQYKLLIGFVWVTSALVALPLLFAMGTEYPLVNP 185
DB 159 VASLSVERYALCHPFRYKAVSGPCQYKLLIGFVWVTSALVALPLLFAMGTEYPLVNP 185
QY 186 HRLGTCRRSTRHHEOPEFETSMGICT--NLSRMTVFOSSTIGARVYLVLSYAFMC 242
DB 211 -----NRKADGQH-----PGGLVCTPYDTATVKKYIQVNTFMSEFLPMLIISLNTYI 259
QY 243 WNMAYVLMSQKSLAGTRPPOLRKSESESESTARRQTIIFLLVYLAVCWMPNQ 300
DB 260 ANKLTVVHQAADQGRGVGVGTH-----NSLEHSTNMSIEPRVQALRHGVLVLA 312
QY 288 IVYTLAVCMPPNDIRIRMAAKPKHDMTRSYFRAYMILLPSETFEYLSVINPLLYTVS 347
DB 313 VVIAFVCMPLPYHVRIMFCYISDEQMTFLFDYHYFMYLNALEYSSAINPLIYNLYV 372
QY 348 SQGFRRVQVLCRLSLQHNHKEKRLVHAHSTDSARFVORPLLFASROSSARREK 407
DB 373 SANRQVFLSTLACLPGRMRKKR-----PTFSKPMSSMSSNAPSTSATRE 421

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ID	NTRI_RAT	STANDARD;	PRT;	424 AA.
NT	NTRI_RAT			
AC	P20769;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1) (HIGH-AFFINITY LEVOACASTINE-SENSITIVE NEUROTENSIN RECEPTOR) (NTRH).			
GN	NTSR1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Rattus			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=90297956; PubMed=1694443;			
RA	Tanaka K., Masu M., Nakanishi S.;			
RT	"Structure and functional expression of the cloned rat neurotensin receptor.";			
RT	Neuron 4:847-854(1990).			
CC	-1- FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	HIGHEST TO TACHIKININS RECEPTORS.			
PIR	JH0164; JH0164.			
DR	GCRD: GCR_0219; "			
DR	GCRD: IPR000276; GPCR_Rhodopsn.			
DR	InterPro: IPR000276; 7tm1_1; 1.			
DR	Pfam: PF00001; 7tm1_1; 1.			
DR	PRINTS: PR00237; GPCRHHODOPSIN.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	phosphorylation; Lipoprotein; Palmitate.			
FT	DOMAIN	1	64	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	65	87	1 (POTENTIAL).
FT	TRANSMEM	88	96	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	97	121	2 (POTENTIAL).
FT	TRANSMEM	122	143	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	144	165	3 (POTENTIAL).
FT	TRANSMEM	166	188	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	189	210	4 (POTENTIAL).
FT	DOMAIN	211	235	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	236	260	5 (POTENTIAL).
FT	TRANSMEM	261	308	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	309	330	6 (POTENTIAL).
FT	DOMAIN	331	348	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	349	372	7 (POTENTIAL).
FT	TRANSMEM	373	424	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	38	38	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	42	42	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	142	225	BY SIMILARITY.
FT	LIPID	388	388	PALMITATE (POTENTIAL).
SO	SEQUENCE	424 AA;	47054 MM;	A9C2P7EAFB9BCD3 CRC64;

	Query Match	20.3%	Score 473;	DB 1;	Length 424;
	Best Local Similarity	30.3%	Pred.	No. 3,9e-28;	
	Matches 118;	Conservative	67;	Mismatches 161;	Indels 44; Gaps 8
Oy	30	KITLLIYLLIFPMGLISATIRTVOLÖKKGY--LOKEVTDHMSLACSDILVFLIGM	87		
	:	: : : :	: : : :	: : : :	: : : :
Dd	64	KVLTAIVLVLFVVGGSNSVT--AFTLARKKSLÖSÖSTVNHNHGISLADSDLITL	121		
Oy	88	PMEYSITIMPLDTSSVYLCKIHPIEFACSYATLLIVLLEFERYALICNHPRYKAYS	147		
	:	: : : :	: : : :	: : : :	: : : :
Dd	122	PVELNTITWNHNMAGDCAQCRKYUTLRACYSATALLANVASLSERTIALCNPPKATLM	161		
Oy	148	GRCOVKLILGFWWTATVAALRDLLEFAMGTETRLVNVPSHRGLTCNRSTRNHQPEPSSNM	207		
	:	: : : :	: : : :	: : : :	: : : :

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Db      182  SRSTKFKFISAIWLASALLAIPLMFLTMGLQ-----NFGSDGTH-----PGG 222
Oy      208  SICINLSRMT--VPOSSIFGAIYVYLVLLVLSAYKFCMMYQYL--KQKQSLA---- 258
Db      223  LVCPIVDTAIVKVVIVQVNFMSFLPEMLVLSINTVIAKLVHQAAEQGVCTGT 282
Oy      259  -GGRPOLRKSESESESRARQFIIFLRILVYLAVCMNPQIRIRLMAAKPRHWDTRS 317
Db      283  HNGLEHSTFNMTIEPRGVQALRHGVLVLRVAIVAVFCWMLPYHRIRLMFCYISDEQWTF 342
Oy      318  YFRAIWMLLPSEFFFLVSLINPLLVSSQQRFRFVQVYOLCRSLQJAHNEKRLRVH 377
Db      343  LFEDYHYFYMLTNALFVSSAINIPLVNLVANSANRQVFLSTLACLCPGMRHRRKKR--- 398
Oy      378  AHSFTDSARFVORPLLPASROSSARRTK 407
Db      399  -----PTFSRKRNMSMSNNAFSTSTRE 421

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	RESULT	4
ID	NTRY_HUMAN	STANDARD; PRT; 418 AA.
AC	P30989;	
AD	01-JUL-1993 (Rel. 26, Created)	
DT	01-JUL-1993 (Rel. 26, Last sequence update)	
DT	20-AUG-2001 (Rel. 40, Last annotation update)	
DE	NEURENENSIN RECEPTOR TYPE 1 (NT-R-1) (HIGH-AFFINITY LEVOCABASTINE-INSENSITIVE NEURENENSIN RECEPTOR) (NTRH).	
GN	NTRH OR NTRR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxId=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93154505; PubMed=8381365;	
RA	Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,	
RA	Gully D., Le Fur G., Ferrara P., Capit D.;	
RT	"Cloning and expression of a complementary DNA encoding a high	
RT	affinity human neurensin receptor.";	
RL	FEST Lett. 317:139-142(1993).	
CC	-I- FUNCTION: RECEPTOR FOR THE TRIDECAPETIDE NEURENENSIN. IT IS ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.	
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.	
CC	-----	
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CC	-----	
DR	EMBL; X70070; CAA9675.1; -.	
DR	PIR; S29506; S29506.	
DR	GCRDB; GCR 0577; -.	
DR	GCRDB; GCR 2067; -.	
DR	MIM; 162651; -.	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PROSITE; PS00237; G_PROTEIN_RECPE_F1.1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_RECPE_F1.2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KW	Phosphorylation; Lipoprotein; Palmitate.	
FT	DOMAIN 1 63 EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 64 86 1 (POTENTIAL).	
FT	DOMAIN 87 95 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 96 120 2 (POTENTIAL).	
FT	DOMAIN 121 142 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 143 164 3 (POTENTIAL).	


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CC EMBL: U51908; AAB17285.1;
DR MGD: MGI:108018; Ntstr2.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.2.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1;
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Lipoprotein; Palmitate.
FT DOMAIN 1 32
FT TRANSMEM 33 55
FT DOMAIN 56 64
FT TRANSMEM 65 87
FT DOMAIN 88 109
FT TRANSMEM 110 131
FT DOMAIN 132 154
FT TRANSMEM 155 176
FT DOMAIN 177 217
FT TRANSMEM 218 238
FT DOMAIN 239 298
FT TRANSMEM 299 319
FT DOMAIN 320 338
FT TRANSMEM 339 359
FT DOMAIN 360 417
FT DISULFID 108 194
FT LIPID 378
SQ SEQUENCE 417 AA; 46537 MW; EBFDDBD6507223DD CRC64;

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Query Match 17.2%; Score 401.5; DB 1; Length 417;

Best Local Similarity 26.9%; Pred. No. 7,6e-23;

Matches 101; Conservative 68; Mismatches 133; Indels 73; Gaps 8;

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OY 28 WITTLIVLIVFVNGLLNSATIRVTVLOKKGVLQKEVDHWSLSPDLVFLIGM 87
DB 30 WAKVETAYKSLIFALGTGNAISVHV--VLAKEGRPRGRKRYHSLSLALLILISV 87
OY 88 PMEFSIINPLTSSYTLCKLHFLPACSAVALLVLLSFERYIAICHPFRKAYS 147
DB 88 PMELYNEVSHYVWFGDLCRGYFVRELCAVAVLSAERCLAVCQPLRRRL 147
OY 148 GPCQVALLIGFWVTALVALPLLFAMGTEYPLVNPVSHRGGLCNRSRHHQEPSTSM 207
DB 148 TPRTKRLSLVWVASLGLAPMAVIMGKHEN-----BRADGEPPAS- 191
OY 208 SICTNLSR-----WTVFQSSIFGAFVYLVLLS----- 237
DB 192 RCTVTVLSRASSSTQVQRAGILRSPLMEL--TAILNGTVNHVALVLSQVVSASQVNS 250
OY 238 -----VAPMCNMNQVLMKKSQKSLAGSTRPPOLRKSSESSESTARRQTIIF 284
DB 251 IPRSLRLSEBGLIGFTW-----RKTLSLGVQASIVRHKDAQSIRSLQNSAQV- 299
OY 285 LRLIVVTLAVCMRNQIRKIMAAAKPKHDTRSYFRAYVILLPESSTFYLSVINPLLY 344
DB 300 LRAIVAVVYICWLPYHARRLMCYIPDDGTDLDYHYFYVWTVTLTFYVSASVTPVLY 359
OY 345 IVSSQOFRFRFVQVL 359
DB 360 NAVSSFRKLFLESL 374

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RESULT 8
GP38 HUMAN STANDARD; PRT; 412 AA.
AC 043193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR38.
GN GPR38
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110578; PubMed=9441746;
RA Hreniuk D.L., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smath R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
RT genes (GPR38 and GPR39) related to the growth hormone secretagogue
RT and neurotensin receptors."
RL Genomics 46:426-434(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THYROID, STOMACH, AND BONE
CC MARROW.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF034632; AAC26081.1;
DR GCRDB: GCR_2494;
DR MIM: 602885;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1.2.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1;
DR PROSITE: PS0262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 74
FT TRANSMEM 75 94
FT DOMAIN 95 112
FT TRANSMEM 113 134
FT DOMAIN 135 157
FT TRANSMEM 158 178
FT DOMAIN 179 246
FT TRANSMEM 247 270
FT DOMAIN 271 298
FT TRANSMEM 299 320
FT DOMAIN 321 334
FT TRANSMEM 335 358
FT DOMAIN 359 412
FT DISULFID 111 235
FT CARBOHYD 6
FT CARBOHYD 192
SQ SEQUENCE 412 AA; 45344 MW; C13FF6165012DER3 CRC64;

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Query Match 15.2%; Score 355.5; DB 1; Length 412;

Best Local Similarity 28.5%; Pred. No. 1,9e-19;

Matches 111; Conservative 65; Mismatches 169; Indels 45; Gaps 13;

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OY 4 PSLPESD---CSQIIDSHVPEFVATWIKITLLVLIIFVWGLNSATIRVTVLOK 60
DB 20 PALPPCDERRCS-----PPLGALVPT--AVCLCFVGVSNVTV--MLGR 65
OY 61 KGYLOKEVTDHNVSLACSDILVFLIGMPMEFYSLINPLTSSYTLCKLHFLFEACSY 120
DB 66 YRDMRTTNILVLSMAVSDLLI-LGLPFLDYR-LMSRPVFPGLLCRLSLVYGECTY 123
OY 121 ATLHLVTLSEFERYIAICHPRYKAVSGPOVKLLIGFWVTALVALPLLFAMGTEY-P 179
DB 124 ATLHLMTLSVEREYIAICRPLARVLTTRRRVALLVLAVALLSAGPLFLVGEVQDP 183
OY 180 LVN-VPSHRLGLCNRSRHHQ-----PESNMSICTNLSRMTVPOSS 223
DB 184 GISVPPGLNGTARIASSPLASPLMLSRAPPSPSPGPTAAALFSSRECRPSPAQ-- 241

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QY 224 IFGAFVYLVLLSVAFPCMMNOVLKSKGSLAGTRPPOLKSESESRAROTII 283
 DB 242 -LGALRLVLMWYTAFFFLPCLSLTYGLIGRELWSSRRP--LGGPAAAGREGRHROTIVR 298
 QY 284 FLRLVYLVAVLWCMMPNQRIRMAAAKPKHDWTRSFYRMYLLPFSEFFYLLSSVIMPL 343
 DB 299 VLLVYLVAFILICMPLFVHGRILYIYI--NTEDSRMATFSQYFNIVALQ--LFLYLSASINPIL 354
 QY 344 YTVSSQDFRFRVVOYLCCRLSLQHANHEKR 373
 DB 355 YNLISKYRAAFKLLARKSRPRGFHRSR 384

RESULT 9
 GHSR_PIG STANDARD; PRT; 366 AA.
 AC 095254; 095255;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING PEPTIDE RECEPTOR) (GHRP).
 GN GHSR.
 OS Sus. scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YORKSHIRE; TISSUE-Pituitary;
 RX MEDLINE=96337998; PubMed=8688086;
 RA Howard A.D., Feighner S.D., Cully D.F., Arena J.P., Liberator P.A., Rosenblum C.L., Hamelin M., Hreniuk D.L., Palyna O.C., Anderson J., Parese P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S., Chaug L.-Y., Elbrecht A., Deskevitz M., Heavens R., Rigby M., Strinathsinghji D.J.S., Dean D.C., Mellillo D.G., Patchett A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;
 RA A receptor in pituitary and hypothalamus that functions in growth hormone release.
 RT Science 273:974-977(1996).
 RL -1- FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS WELL AS NON-PEPTIDE, LOW MOLECULAR WEIGHT SECRETAGOGUES (E.G. L-692,429, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11 PROTEINS. BINDING POTENCY FOR THE SECRETAGOGUES IS IN THE ORDER: MK-0677 > GHRP-2 > GHRP-6.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERE) AND 1B; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B APPEARS NOT TO BIND SECRETAGOGUES.
 CC -1- TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC EMBL: U60178; AAC48630.1; -
 CC EMBL: U60180; AAC48631.1; -
 DR GCRDB: GCR_1537; -
 DR GCRDB: GCR_1538; -
 DR InterPro: IPR003905; GHS1_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Alternative splicing.

FT DOMAIN 1 40
 FT TRANSMEM 41 66
 FT DOMAIN 67 72
 FT TRANSMEM 73 96
 FT DOMAIN 97 117
 FT TRANSMEM 118 139
 FT DOMAIN 140 162
 FT TRANSMEM 163 183
 FT DOMAIN 184 211
 FT TRANSMEM 212 235
 FT DOMAIN 236 263
 FT TRANSMEM 264 285
 FT DOMAIN 286 302
 FT TRANSMEM 303 326
 FT DOMAIN 327 366
 FT DISULFID 116 198
 FT CARBOHYD 13 13
 FT CARBOHYD 27 27
 FT VARSPPLIC 266 289
 FT VARSPPLIC 290 366
 FT SEQUENCE 366 AA; 41194 MR; 2C850B3BF61B7C1C CRC64;

Query Match 13.3%; Score 310; DB 1; Length 366;
 Best Local Similarity 27.8%; Pred. No. 4e-16;
 Matches 95; Conservative 68; Mismatches 139; Indels 40; Gaps 12;

QY 20 VPFEVATWIKITLILYLVIFVWGLGNSATIRVTVOLKQKGLQKEVDHMYSLACSD 79
 DB 35 LPLPEPTPLAGVATVCAVL--FVVGAGNLTMLTVSRFR--WRRTNLYSSMAFSD 89
 QY 80 ILVFLGMPMEFYSLINPNLTSSYTLCKLHFLPFCASVATLLHVLTFERYIAIC 139
 DB 90 LILFLIC-MPDLFR-LWQYRWNLGNLLCKLFQGVSSCJATVLTALTSVEFYAICF 147
 QY 140 PFRYKAVSGPCQVKLLIGFVWVTSALVALPLFLPMGTEPYLVNVPNSHRLGTCNNSSTRHH 199
 DB 148 PLRAKVVTKRGVRLVLIWAVAFCSAGPIFLVGEHD-----NCTDRDT 195
 QY 200 EDPETSNMSTCNLSRRTVPOSSIFGAFVY--LVLLSVAFMCMNMNOVLKSKGSLA 258
 DB 196 NECRATERAVNSGLT-VWVWVSFFFLPVFCULVYSL-----IGKIMRRKREGEA 248
 QY 259 GTRPPOLKSESESRARAROTIIFRLIVTVLAVCMMPNQRIRMAAAKPKHDWTR-S 317
 DB 249 VGS---SLRDQ-----HKQYKMLAVVFAFLICWLPVHGRILYFSKLEPGSYEIA 298
 QY 318 YFRAYMILPFSEFFYSSVINPLTVSSQDFRFRVVOYL 359
 DB 299 QTSQYCNLVSF--VLEVLAAINPLILNIMSKRYRAVAVFKLL 338

RESULT 10
 GHSR_RAT STANDARD; PRT; 364 AA.
 AC 008725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DT GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING PEPTIDE RECEPTOR) (GHRP).
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pituitary;
 RX MEDLINE=97246555; PubMed=9092793;
 RA McKee K.K., Palyna O.C., Feighner S.D., Hreniuk D.L., Tan C., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;

RT "Molecular analysis of rat pituitary and hypothalamic growth hormone
secretagogue receptors." RT
RL Mol. Endocrinol. 11:415-423(1997).
RN [2]
RP SEQUENCE OF 1-240 FROM N.A.
RC STRAIN-MISTAR; TISSUE-Pituitary;
RX MEDLINE=98100386; PubMed=9437732;
RA Yokote R., Sato M., Matsubara S., Ohye H., Nimi M., Murao K.,
Takahara J.;
RT "Molecular cloning and gene expression of growth hormone-releasing
peptide receptor in rat tissues." RT
RL Peptides 19:15-20(1998).
CC -1- FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS
WELL AS NON-PEPTIDE, LOW MOLECULAR WEIGHT SECRETAGOGUES (E.G. L-
692,429, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11
PROTEINS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC "This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch)."
CC EMBL: U094321; AAC53156.1; -
DR EMBL: AB001982; BAA21777.1; ALT_INIT.
DR GCRDB: GCR_1383; -
DR InterPro: IPR003905; GHS1_rcptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PRO0237; GPCRHOOPS.
DR PROSITE: PS00237; G.PROTEIN.RECP.F1.1; 1.
DR PROSITE: PS00262; G.PROTEIN.RECP.F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 40
FT TRANSMEM 41 66
FT DOMAIN 67 72
FT TRANSMEM 73 96
FT DOMAIN 97 117
FT TRANSMEM 118 139
FT DOMAIN 140 162
FT TRANSMEM 163 183
FT DOMAIN 184 211
FT TRANSMEM 212 235
FT DOMAIN 236 263
FT TRANSMEM 264 285
FT DOMAIN 286 302
FT TRANSMEM 303 326
FT DOMAIN 327 364
FT DISULFID 115 197
FT CARBOHYD 13 13
FT CARBOHYD 26 26
SQ SEQUENCE 364 AA; 40963 MW; DCF559B061EE9 CRC64;

Query Match 13.2%; Score 308; DB 1; Length 364;
Best Local Similarity 26.5%; Pred. No. 5,7e-16;
Matches 96; Conservative 71; Mismatches 137; Indels 58; Gaps 13;

QY 7 PGSDCSQIIDHSHVEFEVATWIKITLLIVYIIIVMGLNSATIRYTOVLQKKGYLQK 66
DB 24 PGDSDS---LPDELPLFPAPLAGVATCAVAL--FVVGISGMLTMLVVSRRF---LRT 75
QY 67 EYDHWASLACSDIIVFLGMPMEFYSIINWPLTSSYTLCKHTPLFEACSVATLHV 126
DB 76 TIRLYISSAFSDLLFLFC-MPLDLVR-LMORYPMWFGDLCKLQFVSESCYATVTLTI 133
QY 127 LTLSEFRYTAICHPFRKAVSGPCQKLLIGFVWYTSALVALPLFLFACTEYPLNVDSH 186
DB 134 TALSVERRYFAICPLPRAKVYVTKGRKVLIVYIMVAFCSAGPIVIVGVEHE----- 186

QY 187 RLQTCNRSSRTHHEQPEPSNMSICTNLSSRWTFQSSIFGAFVYLVLLVSAPFCNNMM 246
DB 187 -----NGTDPRNTNCRATFEFAVRSGLLT-VMWVSSVFLEPFCILVL-----YSLI 234
QY 247 OVLKMSQKSLAGGTRPOLKRSSESESRAROTIIFRLIVTVLAVCMPIORRIMA 306
DB 235 GKRLMRRRGDAVGA---SLRDON-----HKQTVKMLAVVFAFILCMLPFHVGRYL- 283
QY 307 AAKPHDMTRF-----FRAMILLPSEFFYLISSINPLTVSSQCFRRFVQ 357
DB 244 -----FSKSEPSGLIEIAISOYCNLVSE--VLFIYSAINPILYINMSKRYAVAFK 334
QY 358 VL 359
DB 335 LL 336

RESULT 11
GHSR_HUMAN
ID GHSR_HUMAN STANDARD; PRT; 366 AA.
AC Q92847; Q92848;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING
PEPTIDE RECEPTOR) (GHRP).
GN GHSR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Pituitary;
RX MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Feigheuer S.D., Cully D.F., Arena J.P.,
RA Liberator P.A., Rosenblum C.I., Hamelin M., Hreniuk D.L.,
RA Palaya O.C., Anderson J., Pareiss P.S., Diaz C., Chou M., Liu K.K.,
RA McKee K.K., Pong S.-S., Chang L.-Y., Elbrecht A., Dashkevicz M.,
RA Heavens R., Rigby M., Sirinathsinghji D.J.S., Dean D.C., Melillo D.G.,
RA Patchett A.A., Nayund R., Griffin P.R., Demartino J.A., Gupta S.K.,
RA Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;
RT "A receptor in pituitary and hypothalamus that functions in growth
hormone release." RT
RL hormone release." RT
CC -1- FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS
WELL AS NON-PEPTIDE, LOW MOLECULAR WEIGHT SECRETAGOGUES (E.G. L-
692,429, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11
PROTEINS. POTENCY RANKING FOR SECRETAGOGUE INHIBITION IS MK-0677
> GHRP-2 > GHRP-6.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERE) AND 1B; ARE
PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B APPEARS NOT TO BIND
SECRETAGOGUES.
CC -1- TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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or send an email to license@isb-sib.ch)."
CC EMBL: U06189; AAC50653.1; -
DR EMBL: U06181; AAC50654.1; -
DR GCRDB: GCR_1917; -
DR GCRDB: GCR_1918; -
DR MIM: 601898; -
DR InterPro: IPR003905; GHS1_rcptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.

DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein;
 KW Alternative splicing.
 FT DOMAIN 1 40
 FT TRANSSEM 41 66
 FT TRANSSEM 67 72
 FT TRANSSEM 73 96
 FT TRANSSEM 97 117
 FT TRANSSEM 118 139
 FT TRANSSEM 140 162
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Db 257 FALCAMPYHLVKTLYMGLSLHWPCEDFLFLMNVFPCICISIVNSCLNPLFLYAFDPFR 316
QY 352 RRYEVOYLCC 361
Db 317 ROACTSMGCC 326

RESULT 13
APJ_HUMAN STANDARD; PRT; 380 AA.
ID APJ_HUMAN
AC P35414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, last sequence update)
DT 20-AUG-2001 (Rel. 40, last annotation update)
DE PROBABLE G-PROTEIN-COUPLED RECEPTOR APJ.
GN AGTRL1 OR APJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;

RA "A human gene that shows identity with the gene encoding the
RT angiotensin receptor is located on chromosome 11."
RL Gene 136:355-360(1993).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.
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CC or send an email to license@isb-sib.ch).
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DR EMBL: U03642; AAA18954.1; -
DR GCRdb; GCR_0806; -
DR MIM: 600052; -
DR InterPro: IPR003904; APJ_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PRO0001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 26
FT TRANSMEM 27 51
FT TRANSMEM 52 66
FT TRANSMEM 67 91
FT DOMAIN 92 100
FT TRANSMEM 101 125
FT DOMAIN 126 144
FT TRANSMEM 145 166
FT DOMAIN 167 200
FT TRANSMEM 201 221
FT TRANSMEM 222 244
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FT TRANSMEM 285 308
FT DOMAIN 309 380
FT CARBOHYD 15 15
FT CARBOHYD 175 175
SQ SEQUENCE 380 AA; 42660 MW; 78DB18BEA6D2B2E4 CRC64;

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Best Local Similarity 24.6%; Pred. No. 2.5e-13;
Matches 91; Conservative 62; Mismatches 154; Indels 63; Gaps 14;

QY 8 GSDCSQIIDHSHVPEEVAWIKITLIL--VYLIFVGLGNSATIRVTOLOKKGTLQ 65
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Db 4 GGDFFNYGADNQSECEYTDKSSGALIPALYMLVFLGTTGNGLVL--WTFVSREKR 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 KEVTHMWSLACSDILVLLIGMPMEFYSLINPLTSSY-----TLCKLTFEPCASY 120
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Db 62 RSADIFIASLAVAD-LTEVVTLP-----LMATYTRDMDPFGTFCKLSSYLIFVNM 114
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 ATLLHVLTFSEFYTAICHP-----FRYKAVSGCQVLLIGFVMSALVALPLPAMG 175
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Db 115 ASVPELTGSLSPRYLAIRPANNALRLR-VSGAVATVVL-----VWLAALLAMVY-VLR 168
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QY 176 TEYPLVNPVSHRGILTCNRSSTRHEDPETSNMISCTNLSHWT---VFOSSIFGARVY 231
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Db 169 TTGDELNTTK--VQC-----YNDYSMAVATVSEMAVEGVGSSTVVGVRVP 213
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 222 LVVLISVAFMCMNMQVLMKSGKSLAGTTRPPQLRSESESESTARAROTIFRLIVPT 291
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Db 214 FTIMLTCTFEFT-----AQTLAGHR-----KERIEGLKRRRLISTIVLVLT 256
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 LAVCMPPNQIRIMAAAKPKHDWTRSYRAYVILLPESEFFLYSVINPLLYTVSSQCF 351
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 257 FALCAMPYHLVKTLYMGLSLHWPCEDFLFLMNVFPCICISIVNSCLNPLFLYAFDPFR 316
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QY 352 RRYEVOYLCC 361
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Db 317 ROACTSMGCC 326

RESULT 14
APJ_MOUSE STANDARD; PRT; 377 AA.
ID APJ_MOUSE
AC Q9WV08;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, last sequence update)
DT 20-AUG-2001 (Rel. 40, last annotation update)
DE PROBABLE G-PROTEIN-COUPLED RECEPTOR APJ (MSR).
GN AGTRL1 OR APJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Rizzoti K.;
RT "The G protein-coupled receptor msr/APJ is expressed in endothelial
RT precursors."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: AJ007612; CAB50696.1; -
DR MGD; MGI:1346086; Agtrl1.
DR InterPro: IPR003904; APJ_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 24

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Query Match 11.7%; Score 272.5; DB 1; Length 380;

Db 354 YANSAMPITYNFLSGKFRREFKAFSCCCLGVHHROEDRLTR----- 396
QY 393 LFASRROSSARTFKIFLSTFQSEAEPOSKOSLLESLPNSGAKP 439
Db 397 --GRTSTESRKSILTQISNFDNISKLSQOYVLTSTLPAANGAP 440

Search completed: January 8, 2002, 23:10:35
Job time: 385 sec